SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Breece, Tim
Hayenga, Kirk
Rinderknecht, Ernst
Vandlen, Richard
Yansura, Daniel

(ii) TITLE OF INVENTION: PROCESS FOR PRODUCING RELAXIN

(iii) NUMBER OF SEQUENCES: 40

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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/080,354
(B) FILING DATE: 21-JUN-1993
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
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(B) REGISTRATION NUMBER: 24,190
(C) REFERENCE/DOCKET NUMBER: A-58117/WHD

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Ser Trp Met Glu Glu Val Ile Lys Leu Cys Gly Arg Glu Leu Val
1 5 10 15

Arg Ala Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser
20 25

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Lys Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

B' cont.

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Thr
1 5 10 15

Lys Arg Ser Leu Ala Arg Phe Cys
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Lys Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Arg Arg Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Lys Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

B' cont.

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Arg Arg Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
ATG AAA AAG AAT ATC GCA TTT CTT CTT AAA CGG GAC TCA TGG ATG GAG        48
Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Arg Asp Ser Trp Met Glu
 1               5                  10                  15

GAA GTT ATT AAA TTA TGC GGC CGC GAA TTA GTT CGC GCG CAG ATT GCC        96
Glu Val Ile Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala
            20                  25                  30
```

```
ATT TGC GGC ATG AGC ACC TGG AGC AAA AGG AAA CCC ACT GGT TAT GGT        144
Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Lys Pro Thr Gly Tyr Gly
          35                  40                  45

TCT CGA AAA AAG AGA CAA CTC TAC AGT GCA TTG GCT AAT AAA TGT TGC        192
Ser Arg Lys Lys Arg Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys
      50                  55                  60

CAT GTT GGT TGT ACC AAA AGA TCT CTT GCT AGA TTT TGC                231
His Val Gly Cys Thr Lys Arg Ser Leu Ala Arg Phe Cys
 65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 593 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 431..586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

B' cont.

```
GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA       60

GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAA GAACTGTGTG CGCAGGTAGA      120

AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG      180

GTTGATTGAT CAGGTAGAGG GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA      240

CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA      300

AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT      360

TGTTTTTATT TTTTAATGTA TTTGTACGCA AGTTCACGTA AAAAGGGTAT CTAGAGGTTG      420

AGGTGATTTT ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC          469
          Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe
            1               5                  10

GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA GAC TCA TGG ATG GAG GAA        517
Val Phe Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ser Trp Met Glu Glu
     15                  20                  25

GTT ATT AAA TTA TGC GGC CGC GAA TTG GTA CGC GCG CAA ATA GCG ATA        565
Val Ile Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile
 30                  35                  40                  45

TGC GGT ATG AGT ACA TGG AGT TGAAGAA                                   593
Cys Gly Met Ser Thr Trp Ser
                50
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 438..1238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
GAATTCAACT TCTCCATACT TGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA      60

GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAA GAACTGTGTG CGCAGGTAGA     120

AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG     180

GTTGATTCAT CAGGTAGAGG GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA     240

CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA     300

AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT     360

TGTTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT TCACGTAAAA AGGGTATCTA     420

GAGGTTGAGG TGATTTT ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT         470
                   Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser
                     1               5                  10

ATG TTC GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA TCA GGC ACT ACA       518
Met Phe Val Phe Ser Ile Ala Thr Asn Ala Tyr Ala Ser Gly Thr Thr
            15                  20                  25

AAT ACT GTG GCA GCA TAT AAT TTA ACT TGG AAA TCA ACT AAT TTC AAG       566
Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys
        30                  35                  40

ACA ATT TTG GAG TGG GAA CCC AAA CCC GTC AAT CAA GTC TAC ACT GTT       614
Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val
    45                  50                  55

CAA ATA AGC ACT AAG TCA GGA GAT TGG AAA AGC AAA TGC TTT TAC ACA       662
Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr
60                  65                  70                  75

ACA GAC ACA GAG TGT GAC CTC ACC GAC GAG ATT GTG AAG GAT GTG AAG       710
Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys
                80                  85                  90

CAG ACG TAC TTG GCA CGG GTC TTC TCC TAC CCG GCA GGG AAT GTG GAG       758
Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu
            95                  100                 105

AGC ACC GGT TCT GCT GGG GAG CCT CTG TAT GAG AAC TCC CCA GAG TTC       806
Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe
        110                 115                 120

ACA CCT TAC CTG GAG ACA AAC CTC GGA CAG CCA ACA ATT CAG AGT TTT       854
Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe
    125                 130                 135

GAA CAG GTG GGA ACA AAA GTG AAT GTG ACC GTA GAA GAT GAA CGG ACT       902
Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr
140                 145                 150                 155

TTA GTC AGA AGG AAC AAC ACT TTC CTA AGC CTC CGG GAT GTT TTT GGC       950
Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly
                160                 165                 170
```

```
AAG GAC TTA ATT TAT ACA CTT TAT TAT TGG AAA TCT TCA AGT TCA GGA        998
Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly
            175                 180                 185

AAG AAA ACA GCC AAA ACA AAC ACT AAT GAG TTT TTG ATT GAT GTG GAT       1046
Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp
        190                 195                 200

AAA GGA GAA AAC TAC TGT TTC AGT GTT CAA GCA GTG ATT CCC TCC CGA       1094
Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg
    205                 210                 215

ACA GTT AAC CGG AAG AGT ACA GAC AGC CCG GTA GAG TGT ATG GGC CAG       1142
Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln
220                 225                 230                 235

GAG AAA GGC CAA TTC AGA GAA ATA TTC TAC ATC ATT GGA GCT GTG GTA       1190
Glu Lys Gly Gln Phe Arg Glu Ile Phe Tyr Ile Ile Gly Ala Val Val
                240                 245                 250

TTT GTG GTC ATC ATC CTT GTC ATC ATC CTG GCT ATA TCT CTA CAC TAAAATTCTC   1245
Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile Ser Leu His
            255                 260                 265

ATGTTTGACA GCTTATCATC GATAAGCTTT AATGCGGTAG TTTATCACAG TTAAATTGCT     1305

AACGCAGTCA GGCACCGTGT ATGAAATCTA ACAATGCGCT CATCGTCATC CTCGGCACCG     1365

TCACCCTGGA TGCTGTAGGC ATAGGCTTGG TTATGCCGGT ACTGCCGGGC CTCTTGCGGG     1425

ATATCGTCCA TTCCGACAGC ATCGCCAGTC ACTATGGCGT GCTCCTAGCG CTATATGCGT     1485

TGATGCAATT TCTAT                                                      1500
```

B' cont-

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Met Lys Lys Asn Ile Ala Phe Leu Leu Arg Lys
  1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Met Lys Lys Asn Ile Ala Phe Leu Leu Arg Arg
  1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 5..42
(D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 5 and 42 to SEQ ID NO:16. "

B' cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTAGAATTAT GAAAAAGAAT ATCGCATTTC TTCTTAAACG GG 42

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 4..41
(D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 4 and 41 to SEQ ID NO:15."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGTCCCGTTT AAGAAGAAAT GCGATATTCT TTTTCATAAT T 41

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 5..42
(D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 5 and 42 to SEQ ID NO:18."

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 9..41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
CTAGAATT ATG TTC CCA GCT ATG CCT CTA TCT AGT AAA CGG G                42
         Met Phe Pro Ala Met Pro Leu Ser Ser Lys Arg
           1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

B' cont.

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 4..41
(D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 4 and 41 to SEQ ID NO:17."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
AGTCCCGTTT ACTAGATAGA GGCATAGCTG GGAACATAAT T                        41
```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Met Phe Pro Ala Met Pro Leu Ser Ser Lys Arg
 1           5                  10
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 5..64

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 5..64
(D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 5 and 64 to SEQ ID NO:21."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
CGCG CAG ATT GCC ATT TGC GGC ATG AGC ACC TGG AGC AAA AGG AAA CCC      49
     Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Lys Pro
       1               5                  10                  15

ACT GGT TAT GGT TCT                                              64
Thr Gly Tyr Gly Ser
                20
```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

B' cont.

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 3..62
(D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 3 and 62 to SEQ ID NO:20."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
CGAGAACCAT AACCAGTGGG TTTCCTTTTG CTCCAGGTGC TCATGCCGCA AATGGCAATC      60

TG                                                                     62
```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Lys Pro Thr
  1               5                  10                  15

Gly Tyr Gly Ser
            20
```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 5..50
(D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 5 and 50 with SEQ ID NO:24."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCCACTCTG TGCGGTGCTG AACTGGTTGA CGCTCTGCAG TTTGTTTGCG 50

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 6..50
(D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 6 and 50 with SEQ ID NO:23."

B' cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTCACCGCAA ACAAACTGCA GAGCGTCAAC CAGTTCAGCA CCGCAAGAGT 50

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..55
(D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 1 and 55 with SEQ ID NO:26."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTCCCGAAA CTCTGTGCGG TGCTGAACTG GTTGACGCTC TGCAGTTTGT TTGCG 55

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 6..64
(D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 6 and 64 with SEQ ID NO:25."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCACCGCAA ACAAACTGCA GAGCGTCAAC CAGTTCAGCA CCGCACAGAG TTTCGGGACC 60

TGCA 64

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 5..84
(D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 5 and 84 with SEQ ID NO:28."

B' cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTAGAATTAT GATGATTACT CTGCGCAAAC TTCCTCTGGC GGTTGCCGTC GCAGCGGGCG 60

TAATGTCTGC TCAGGCCATG GCCA 84

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 5..84
(D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 5 and 84 with SEQ ID NO:27."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GATCTGGCCA TGGCCTGAGC AGACATTACG CCCGCTGCGA CGGCAACCGC CAGAGGAAGT 60

TTGCGCAGAG TAATCATCAT AATT 84

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..52
(D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 1 and 52 with SEQ ID NO:30."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAACTCTACA GTGCATTGGC TAATAAATGT TGCCATGTTG GTTGTACCAA AA 52

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

B' cont

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 5..56
(D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 5 and 56 with SEQ ID NO:29."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCTTTTGG TACAACCAAC ATGGCAACAT TTATTAGCCA ATGCACTGTA GAGTTGTGCA 60

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Arg Arg Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Lys Lys Arg
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Arg Arg Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: protein

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Arg Asp Ser Trp Met Glu
 1               5                  10                  15

Glu Val Ile Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala
            20                  25                  30

Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Lys Pro Thr Gly Tyr Gly
        35                  40                  45

Ser Arg Lys Lys Arg Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys
    50                  55                  60

His Val Gly Cys Thr Lys Arg Ser Leu Ala Arg Phe Cys
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```
GC GGC CGC GAA TTA GTT CGC GCG CAG ATT GCC ATT TGC GGC ATG AGC          47
   Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile Cys Gly Met Ser
     1               5                  10                  15

ACC TGG AGC AAA AGG TCT CTG AGC CAG GAA GAT GCT CCT CAG ACA CCT          95
Thr Trp Ser Lys Arg Ser Leu Ser Gln Glu Asp Ala Pro Gln Thr Pro
                20                  25                  30

AGA CCA GTG GCA GAA ATT GTG CCA TCC TTC ATC AAC AAA GAT ACA GAA          143
Arg Pro Val Ala Glu Ile Val Pro Ser Phe Ile Asn Lys Asp Thr Glu
            35                  40                  45

ACC ATA AAT ATG ATG TCA GAA TTT GTT GCT AAT TTG CCA CAG GAG CTG          191
Thr Ile Asn Met Met Ser Glu Phe Val Ala Asn Leu Pro Gln Glu Leu
        50                  55                  60

AAG TTA ACC CTG TCT GAG ATG CAG CCA GCA TTA CCA CAG CTA CAA CAA          239
Lys Leu Thr Leu Ser Glu Met Gln Pro Ala Leu Pro Gln Leu Gln Gln
    65                  70                  75

CAT GTA CCT GTA TTA AAA GAT TCC AGT CTT CTC TTT GAA GAA TTT AAG          287
His Val Pro Val Leu Lys Asp Ser Ser Leu Leu Phe Glu Glu Phe Lys
80                  85                  90                  95

AAA CTT ATT CGC AAT AGA CAA AGT GAA GCC GCA GAC AGC AGT CCT TCA          335
Lys Leu Ile Arg Asn Arg Gln Ser Glu Ala Ala Asp Ser Ser Pro Ser
                100                 105                 110

GAA TTA AAA TAC TTA GGC TTG GAT ACT CAT TCT CGA AAA AAG AGA CAA          383
Glu Leu Lys Tyr Leu Gly Leu Asp Thr His Ser Arg Lys Lys Arg Gln
            115                 120                 125

CTC TAC AGT GCA TTG GCT AAT AAA TGT TGC CAT GTT GGT TGT ACC AAA          431
Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Thr Lys
        130                 135                 140

AGA TCT CTT GCT AGA TTT TGC TGAGATGAAG CTAATTGTGC ACATCTCGTA             482
Arg Ser Leu Ala Arg Phe Cys
    145                 150

TAATATTCAC ACATATTCTT AATGACATTT CACTGATGCT TCTATCAGGT CAATTCTCAT        542

GTTTGACAGC TTATCATCGA TAAGCTTTAA TGCGGTAGTT TATCACAGTT AAATTGCTAA        602

CGCAGTCAGG CACCGTGTAT GAAATCTAAC AATGCGCTCA TCGTCATCCT CGGCACCGTC        662

ACCCTGGATG CTGTAGGCAT AGGCTTGGTT ATGCCGGTAC TGCCGGGCCT CTTGCGGGAT        722

ATCGTCCATT CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGCT ATATGCGTTG        782

ATGCAATTTC TATGCGCACC CGTTCTCGGA GCACTGTCCG ACCGCTTTGG CCGCCGCCCA        842

GTCCTGCTCG CTTCGCTACT TGGAGCCACT ATCGACTACG CGATCATGGC GACCACACCC        902

GTCCTGTGGA TCC                                                          915
```

B' cont.

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile Cys Gly Met Ser Thr
 1               5                  10                  15

Trp Ser Lys Arg Ser Leu Ser Gln Glu Asp Ala Pro Gln Thr Pro Arg
            20                  25                  30

Pro Val Ala Glu Ile Val Pro Ser Phe Ile Asn Lys Asp Thr Glu Thr
        35                  40                  45

Ile Asn Met Met Ser Glu Phe Val Ala Asn Leu Pro Gln Glu Leu Lys
    50                  55                  60

Leu Thr Leu Ser Glu Met Gln Pro Ala Leu Pro Gln Leu Gln Gln His
65                  70                  75                  80

Val Pro Val Leu Lys Asp Ser Ser Leu Leu Phe Glu Glu Phe Lys Lys
                85                  90                  95

Leu Ile Arg Asn Arg Gln Ser Glu Ala Ala Asp Ser Ser Pro Ser Glu
            100                 105                 110

Leu Lys Tyr Leu Gly Leu Asp Thr His Ser Arg Lys Lys Arg Gln Leu
        115                 120                 125

Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Thr Lys Arg
    130                 135                 140

Ser Leu Ala Arg Phe Cys
145                 150
```

(2) INFORMATION FOR SEQ ID NO:37:

B' cont.

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser
 1               5                  10                  15

Ile Ala Thr Asn Ala Tyr Ala Asp Ser Trp Met Glu Glu Val Ile Lys
            20                  25                  30

Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile Cys Gly Met
        35                  40                  45

Ser Thr Trp Ser
    50
```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser
 1               5                  10                  15

Ile Ala Thr Asn Ala Tyr Ala Ser Gly Thr Thr Asn Thr Val Ala Ala
            20                  25                  30

Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp
        35                  40                  45

Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr Lys
    50                  55                  60

Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys
65                  70                  75                  80

Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu Ala
                85                  90                  95

Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser Ala
            100                 105                 110

Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu
        115                 120                 125

Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly Thr
    130                 135                 140

Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg Asn
145                 150                 155                 160

Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr
                165                 170                 175

Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala Lys
            180                 185                 190

Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr
        195                 200                 205

Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg Lys
    210                 215                 220

Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys Gly Gln Phe
225                 230                 235                 240

Arg Glu Ile Phe Tyr Ile Ile Gly Ala Val Val Phe Val Val Ile Ile
                245                 250                 255

Leu Val Ile Ile Leu Ala Ile Ser Leu His
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 7..297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
AAGCTT ATG AAA TCT AAC AAT GCG CTC ATC GTC ATC CTC GGC ACC GTC          48
       Met Lys Ser Asn Asn Ala Leu Ile Val Ile Leu Gly Thr Val
         1               5                  10

ACC CTG GAT GCT GTA GGC ATA GGC TTG GTT ATG CCG GTA CTG CCG GGC          96
Thr Leu Asp Ala Val Gly Ile Gly Leu Val Met Pro Val Leu Pro Gly
 15                  20                  25                  30

CTC TTG CGG GAT ATC GTC CAT TCC GAC AGC ATC GCC AGT CAC TAT GGC         144
Leu Leu Arg Asp Ile Val His Ser Asp Ser Ile Ala Ser His Tyr Gly
                 35                  40                  45

GTG CTG CTA GCG CTA TAT GCG TTG ATG CAA TTT CTA TGC GCA CCC GTT         192
Val Leu Leu Ala Leu Tyr Ala Leu Met Gln Phe Leu Cys Ala Pro Val
             50                  55                  60

CTC GGA GCA CTG TCC GAC CGC TTT GGC CGC CGC CCA GTC CTG CTC GCT         240
Leu Gly Ala Leu Ser Asp Arg Phe Gly Arg Arg Pro Val Leu Leu Ala
         65                  70                  75

TCG CTA CTT GGA GCC ACT ATC GAC TAC GCG ATC ATG GCG ACC ACA CCC         288
Ser Leu Leu Gly Ala Thr Ile Asp Tyr Ala Ile Met Ala Thr Thr Pro
     80                  85                  90

GTC CTG TGG ATCC                                                       301
Val Leu Trp
 95
```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```
Met Lys Ser Asn Asn Ala Leu Ile Val Ile Leu Gly Thr Val Thr Leu
 1               5                  10                  15

Asp Ala Val Gly Ile Gly Leu Val Met Pro Val Leu Pro Gly Leu Leu
            20                  25                  30

Arg Asp Ile Val His Ser Asp Ser Ile Ala Ser His Tyr Gly Val Leu
        35                  40                  45

Leu Ala Leu Tyr Ala Leu Met Gln Phe Leu Cys Ala Pro Val Leu Gly
    50                  55                  60

Ala Leu Ser Asp Arg Phe Gly Arg Arg Pro Val Leu Leu Ala Ser Leu
65                  70                  75                  80

Leu Gly Ala Thr Ile Asp Tyr Ala Ile Met Ala Thr Thr Pro Val Leu
                85                  90                  95

Trp
```